Fig. 1

TGGTTGTCCTGGAACTCACTCTGTAGACCAGGCTGGCCATGAACTCACAGA
GATCTACCTCCTGAGTGCTGGGATTAAAGGTTTGTGCCACCACCTCCCAACT
CTAAGGTGTTTCTTTAAGTTAGGGGCATAGTAAACATTGTTGAGATACTAGA
GGAACACTGAATGAAAATTTGGACATCTCTGCTTTAGGTTTGTGCTGAGCA
GTTTGCCTCTTATCTTCACCTATGCTGAAAAGTTTGAGTTCATAATTTTGAA
CATGCATATGATAAAATATTCTGGCCGCACATTGAATAAATATATTTTAAAT
GAACTTACCTTTAAAATGTCAGTAACAACTCTGCATGGTTTTCTTCTTACCT
CCATAGGTATGGTCTGAATATGCGTTGTTTGGCAGCTCGGGTCAACTATAA
GACTTTGATTATCATCTGTGCGCTATTCACTTTGGTCACAGTACTTTTGTGG
AATAAGTGTTCCAGCGACAAAGCAATCCAGTTTCCTCGGCACTTGAGTAGT
GGATTCAGAGTGGATGGATTAGAAAAAAGATCAGCAGCATCTGAAAGTAAC
CACTATGCCAACCACATAGCCAAACAGCAGTCAGAAGAGGCATTTCCTCAG
GAACAACAGAAGGCACCCCCTGTTGTTGGGGGCTTCAATAGCAACGGGGGA
AGCAAGGTGTTAGGGCTCAAATATGAAGAGATTGACTGTCTCATAAACGAT
GAGCACACCATTAAAGGGAGACGAGAGGGGAATGAAGTTTTCCTTCCATTC
ACTTGGGTAGAGAAATACTTTGATGTTTATGGAAAAGTGGTCCGAGTATGA
CGGCTATGATCGATTTGAATTC::TCTCATAGCTATTCCAAAGTCTATGCACAGA
GAGCCCCTTATCACCCTGATGGTGTGTTTATGTCCTTTGAAGGCTACAATGTGGA
AGTCCGAGACAGAGTCAAGTGCATAAGTGGGGTTGAAGGTGTACCTTTATCTACA
CAGTGGGGACCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATGGGTTAA
GTCACTACAGCAAGAATCTAACTGAAAAACCCCCTCATATAGAGGTATATGAAA
CAGCAGAAGACAGGGACAAAAACAGCAAGCCCAATGACTGGACTGTGCCCAAGG
GCTGCTTTATGGCTAGTGTGGCTGATAAGTCAAGATTCACCAATGTTAAACAGTT
CATTGCTCCAGAAACCAGTGAAGGTGTATCCTTGCAACTGGGGAACACAAAAGA
TTTTATTATTTCATTTGACCTCAAGTTCTTAACAAATGGAAGCGTGTCTGTGGTTC
TGGAGACGACAGAAAAGAATCAGCTCTTCACTGTACATTATGTCTCAAATACCCA

FIG. 1 CONT.

GCTAATTGCTTTTAAAGAAAGAGACATATACTATGGCATCGGGCCCAGAACATCA
TGGAGCACAGTTACCCGGGACCTGGTCACTGACCTCAGGAAAGGAGTGGGTCTTT
CCAACACAAAAGCTGTCAAGCCAACAAGAATAATGCCCAAGAAGGTGGTTAGGT
TGATTGCGAAAGGGAAGGGCTTCCTTGACAACATTACCATCTCTACCACAGCCCA
CATGGCTGCCTTCTTCGCTGCCAGTGACTGGCTGGTGAGGAACCAGGATGAGAAA
GGCGGCTGGCCGATTATGGTGACCCGTAAGTTAGGGGAAGGCTTCAAGTCTTTAG
AGCCAGGGTGGTACTCCGCCATGGCCCAAGGGCAAGCCATTTCTACATTAGTCAG
GGCCTATCTCTTAACAAAAGACCATATATTCCTCAATTCAGCTTTAAGGGCAACA
GCCCCTTACAAGTTTCTGTCAGAGCAGCATGGAGTCAAGGCTGTGTTTATGAATA
AACATGACTGGTATGAAGAATATCCAACTACACCTAGCTCTTTTGTTTTAAATGG
CTTTATGTATTCTTTAATTGGGCTGTATGACTTAAAAGAAACTGCAGGGGAAAAA
CTCGGGAAAGAAGCGAGGTCCTTGTATGAGCGTGGCATGGAATCCCTTAAAGCC
ATGCTCCCCTTGTACGACACTGGCTCAGGAACCATCTATGACCTCCGGCACTTCA
TGCTTGGCATTGCCCCCAACCTGGCCCGCTGGGACTATCACACCACCCACATCAA
TCAACTGCAGCTGCTTAGCACCATTGATGAGTCCCCAATCTTCAAAGAATTTGTC
AAGAGGTGGAAGAGCTACCTTAAAGGCAGCCGGGCAAAGCACAACTAG

ATGCGTTGTTTGGCAGCTCGGGTCAACTATAAGACTTTGATTATCATCTGTGCGC
TATTCACTTTGGTCACAGTACTTTTGTGGAATAAGTGTTCCAGCGACAAAGCAAT
CCAGTTTCCTCGGCACTTGAGTAGTGGATTCAGAGTGGATGGATTAGAAAAAAGA
TCAGCAGCATCTGAAAGTAACCACTATGCCAACCACATAGCCAAACAGCAGTCA
GAAGAGGCATTTCCTCAGGAACAACAGAAGGCACCCCCTGTTGTTGGGGGCTTCA
ATAGCAACGGGGGAAGCAAGGTGTTAGGGCTCAAATATGAAGAGATTGACTGTC
TCATAAACGATGAGCACACCATTAAAGGGAGACGAGAGGGGAATGAAGTTTTCC
TTCCATTCACTTGGGTAGAGAAATACTTTGATGTTTATGGAAAAGTGGTCCAGTA
TGACGGCTATGATCGATTTGAATTCTCTCATAGCTATTCCAAAGTCTATGCACAG
AGATCACCTTATCACCCTGACGGTGTGTTTATGTCCTTTGAAGGCTACAATGTGG
AAGTCCGAGACAGAGTCAAATGTATAAGTGGAGTTGAAGGTGTGCCATTATCTAC
CCAGTGGGGGCCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATGGGCTA
AGTCATTACAGCAAGAATCTAACCGAGAAACCCCCTCACATAGAAGTATATGAA
ACAGCAGAAGACAGGGACAGAAACATCAGACCTAATGAATGGACTGTGCCCAAG
GGGTGcttCATGGCCAGTGTGGCAGACAAGTCTAGATCCACCAATGTTAAACAGTT
TATTGCTCCAGAAACCAGTGAAGGTGTGTCTTTGCAGCTGGGAAACACAAAAGAC
TTCATTATTTCATTTGACCTCAAGCTTTTAACAAATGGGAGTGTGTCTGTGGTTCT
GGAGACCACAGAAAAGAATCAGCTCTTCACTGTGCATTATGTCTCAAACACCCAG
CTGATTGCTTTCAGAGACAGGGACATATACTACGGCATTGGGCCCAGAACTTCAT
GGAGTACAGTTACCAGAGACCTGGTCACTGACCTCAGGAAAGGAGTGGGCCTTT
CTAACACAAAAGCTGTCAAGCCAACCAAAATCATGCCCAAAAAGGTGGTTAGGT
TGATTGCAAAAGGGAAGGGATTCCTGGACAACATTACCATCTCAACCACAGCCC
ACATGGCTGCATTCTTTGCTGCAAGTGACTGGCTAGTGAGGAACCAGGATGAGAA
AGGTGgctGGCCAATTATGGTGACCCGGAAGTTAGGGGAAGGGTTTAAATCTTTAG
AACCAGGATGGTACTCTGCCATGGCACAAGGGCAAGCCATCTCTACCTTAGTCAG
GGCCTATCTTCTAACGAAAGACTATGTATTCCTCAGTTCAGCTTTAAGGGCAACA
GCCCCATACAAGTTTCCGTCAGAGCAGCATGGAGTTAAAGCCGTGTTCATGAATA
AACATGACTGGTATGAAGAATATCCAACCACACCTAGCTCTTTTGTTTTAAATGG
CTTTATGTATTCTTTAATTGGGCTGTATGACCTAAAAGAAACAGCAGGGGAGACA

FIG. 2

CTTGGGAAAGAAGCAAGGTCCTTGTACGAGCGCGGCATGGAATCTCTTAAAGCC
ATGCTGCCCTTGTATGATACTGGCTCCGGGACCATCTATGACCTCCGCCACTTCA
TGCTTGGCATTGCTCCCAACCTGGCCCGCTGGGACTATCACACCACCCACATTAA
CCAGCTGCAGCTGCTCAGCACCATCGATGAGTCCCCAATCTTCAAAGAATTTGTC
AAGAGGTGGAAAAGCTACCTTAAAGGCAGTAGGGCAAAGCACAAC

FIG. 2 CONT'D

MetArgCysLeuAlaAlaArgValAsnTyrLysThrLeuIleIleIleCysAlaLeuPheThrLeuValThrValLe
uLeuTrpAsnLysCysSerSerAspLysAlaIleGlnPheProArgHisLeuSerSerGlyPheArgValAspGlyL
euGluLysArgSerAlaAlaSerGluSerAsnHisTyrAlaAsnHisIleAlaLysGlnGlnSerGluGluAlaPheP
roGlnGluGlnGlnLysAlaProProValValGlyGlyPheAsnSerAsnGlyGlySerLysValLeuGlyLeuLy
sTyrGluGluIleAspCysLeuIleAsnAspGluHisThrIleLysGlyArgArgGluGlyAsnGluValPheLeuP
roPheThrTrpValGluLysTyrPheAspValTyrGlyLysValValGlnTyrAspGlyTyrAspArgPheGluP
heSerHisSerTyrSerLysValTyrAlaGlnArgSerProTyrHisProAspGlyValPheMetSerPheGluGly
TyrAsnValGluValArgAspArgValLysCysIleSerGlyValGluGlyValProLeuSerThrGlnTrpGlyPr
oGlnGlyTyrPheTyrProIleGlnIleAlaGlnTyrGlyLeuSerHisTyrSerLysAsnLeuThrGluLysProPro
HisIleGluValTyrGluThrAlaGluAspArgAspArgAsnIleArgProAsnGluTrpThrValProLysGlyC
ysPheMetAlaSerValAlaAspLysSerArgSerThrAsnValLysGlnPheIleAlaProGluThrSerGluGly
ValSerLeuGlnLeuGlyAsnThrLysAspPheIleIleSerPheAspLeuLysLeuLeuThrAsnGlySerValSe
rValValLeuGluThrThrGluLysAsnGlnLeuPheThrValHisTyrValSerAsnThrGlnLeuIleAlaPhe
ArgAspArgAspIleTyrTyrGlyIleGlyProArgThrSerTrpSerThrValThrArgAspLeuValThrAspLe
uArgLysGlyValGlyLeuSerAsnThrLysAlaValLysProThrLysIleMetProLysLysValValArgLeuIl
eAlaLysGlyLysGlyPheLeuAspAsnIleThrIleSerThrThrAlaHisMetAlaAlaPhePheAlaAlaSerA
spTrpLeuValArgAsnGlnAspGluLysGlyGlyTrpProIleMetValThrArgLysLeuGlyGluGlyPheLy
sSerLeuGluProGlyTrpTyrSerAlaMetAlaGlnGlyGlnAlaIleSerThrLeuValArgAlaTyrLeuLeuT
hrLysAspTyrValPheLeuSerSerAlaLeuArgAlaThrAlaProTyrLysPheProSerGluGlnHisGlyVal
LysAlaValPheMetAsnLysHisAspTrpTyrGluGluTyrProThrThrProSerSerPheValLeuAsnGlyP
heMetTyrSerLeuIleGlyLeuTyrAspLeuLysGluThrAlaGlyGluThrLeuGlyLysGluAlaArgSerLe
uTyrGluArgGlyMetGluSerLeuLysAlaMetLeuProLeuTyrAspThrGlySerGlyThrIleTyrAspLeu
ArgHisPheMetLeuGlyIleAlaProAsnLeuAlaArgTrpAspTyrHisThrThrHisIleAsnGlnLeuGlnLe
uLeuSerThrIleAspGluSerProIlePheLysGluPheValLysArgTrpLysSerTyrLeuLysGlySerArgAl
aLysHisAsn

FIG. 3

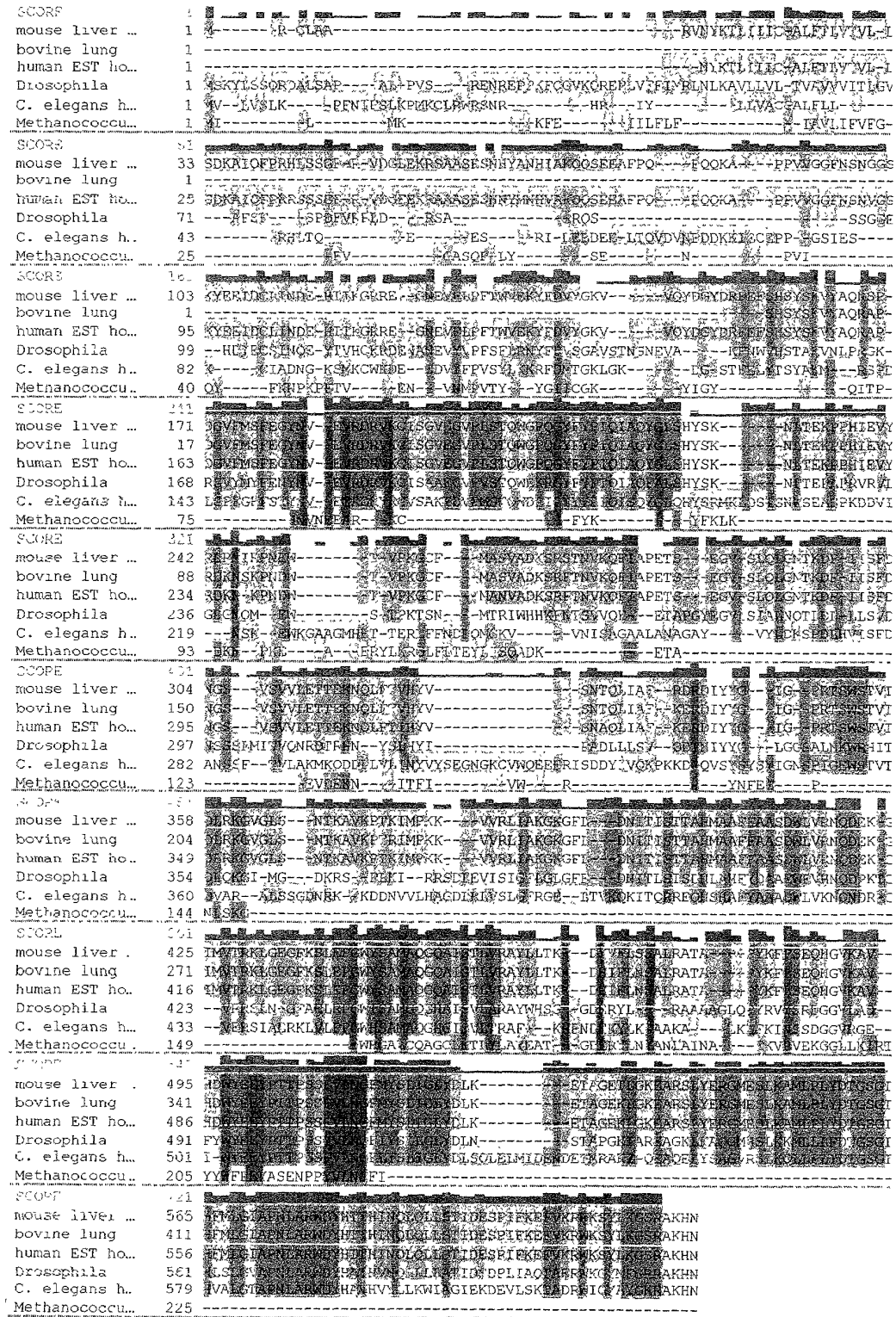
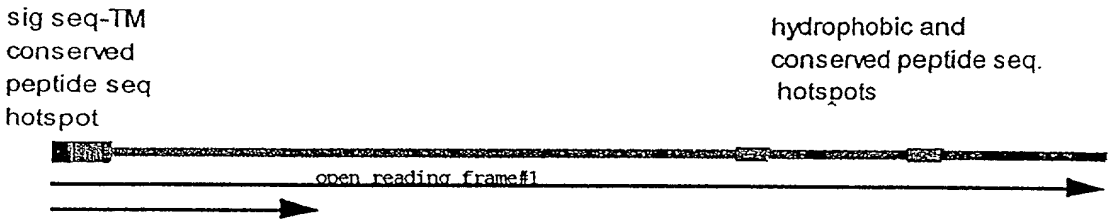


Fig. 4



Hypothetical orientation, **if** inserted into golgi

cytosol->lumen----------->cytosol----->lumen

Key:

signal sequence, highly hydrophobic transmembrane (TM) sequence

Hydrophobic transmembrane (TM) or buried sequence

most conserved peptide sequence (>50% similarity to C elegans 71.9 KD hypothetical protein; 38% similarity to Methanococcus hypothetical protein). Note: peptide identity between mouse, bovine and human > 95%!

Which in text appears:

```
mouse C5-e...    1 MRCLAARVNY KTLIIICALF TLVTVLLWNK CSSDKAIQFP RHLSSGFRVD
                51 GLEKRSAASE SNHYANHIAK QQSEEAFPQE QQKAPPVVGG FNSNGGSKVL
               101 GLKYEEIDCL INDEHTIKGR REGNEVFLPF TWVEKYFDVY GKVVQYDGYD
               151 RFEFSHSYSK VYAQRSPYHP DGVFMSFEGY NVEVRDRVKC ISGVEGVPLS
               201 TQWGPQGYFY PIQIAQYGLS HYSKNLTEKP PHIEVYETAE DRDRNIRPNE
               251 WTVPKGCFMA SVADKSRSTN VKQFIAPETS EGVSLQLGNT KDFIISFDLK
               301 LLTNGSVSVV LETTEKNQLF TVHYVSNTQL IAFRDRDIYY GIGPRTSWST
               351 VTRDLVTDLR KGVGLSNTKA VKPTKIMPKK VVRLIAKGKG FLDNITISTT
               401 AHMAAFFAAS DWLVRNQDEK GGWPIMVTRK LGEGFKSLEP GWYSAMAQGQ
               451 AISTLVRAYL LTKDYVFLSS ALRATAPYKF PSEQHGVKAV FMNKHDWYEE
               501 YPTTPSSFVL NGFMYSLIGL YDLKETAGET LGKEARSLYE RGMESLKAML
               551 PLYDTGSGTI YDLRHFMLGI APNLARWDYH TTHINQLQLL STIDESPIFK
               601 EFVKRWKSYL KGSRAKHN
```

FIG. 5

FIG. 6A

First active tagged recombinant (bovine) C5
(specific activity 5 X 10^5 cpm/mg/h)

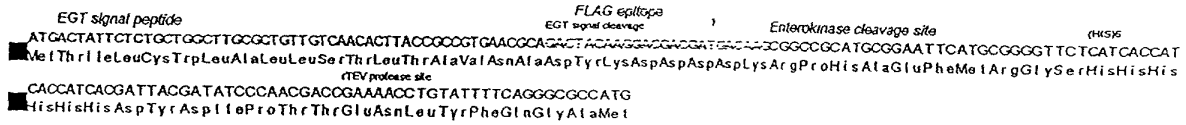
The most active recombinant (full mouse) C5
(specific activity 2 X 10^9 cpm/mg/h)

Chimeric construct
(preliminary data indicate activity is 87% of full mouse):

Truncated mouse
(preliminary data indicate activity is same as first bovine construct):

15

FIG. 6B



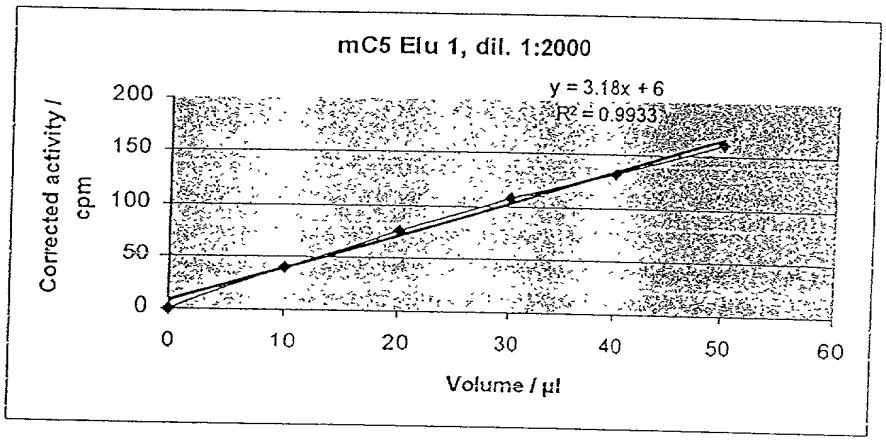

mC5 Elu 1, dil. 1:2000
y = 3.18x + 6
R² = 0.9933
Corrected activity / cpm
200
150
100
50
0
0
10
20
30
40
50
60
Volume / µl

FIG. 7

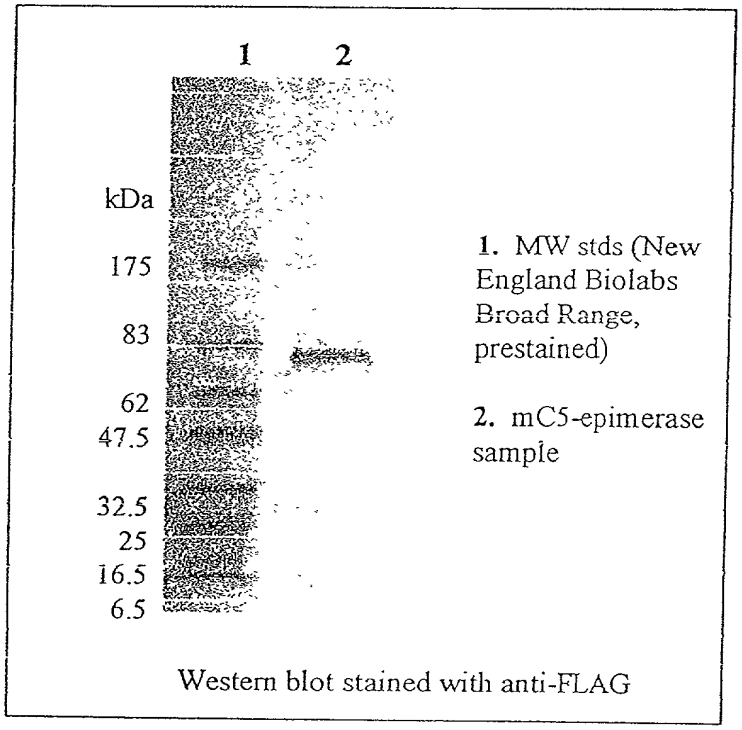

1
2
kDa
175
83
62
47.5
32.5
25
16.5
6.5
1. MW stds (New England Biolabs Broad Range, prestained)
2. mC5-epimerase sample
Western blot stained with anti-FLAG

FIG. 8

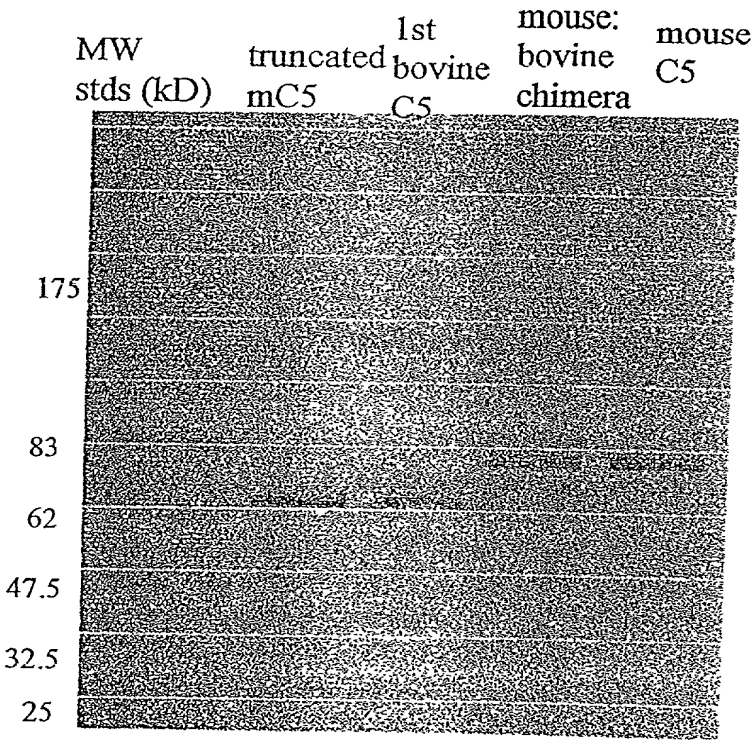

MW stds (kD)
truncated mC5
1st bovine C5
mouse: bovine chimera
mouse C5
175
83
62
47.5
32.5
25

FIG. 9